#### **RAW SEQUENCE LISTING**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number:	10/557,288
Source:	, Py/10
Date Processed by STIC:	11/28/05
	, , , , , , , , , , , , , , , , , , , ,

# ENTERED



PCT

**RAW SEQUENCE LISTING**PATENT APPLICATION: **US/10/557,288**DATE: 11/28/2005

TIME: 13:16:19

Input Set : A:\PTO.TS.txt

```
3 <110> APPLICANT: ENEA-Ente per le Nuove Tecnologie e l'Ambiente
              Consiglio Nazionale delle Ricerche
     6 <120> TITLE OF INVENTION: Method for the preparation of transgenic plants
characterised by
            ' Geminivirus lasting resistance
     9 <130> FILE REFERENCE: PCT25622
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/557,288
C--> 12 <141> CURRENT FILING DATE: 2005-11-17
    14 <150> PRIOR APPLICATION NUMBER: RM2003A000242
    15 <151> PRIOR FILING DATE: 2003-05-19
    17 <160> NUMBER OF SEQ ID NOS: 12
    19 <170> SOFTWARE: PatentIn version 3.2
    21 <210> SEQ ID NO: 1
    22 <211> LENGTH: 630
    23 <212> TYPE: DNA
    24 <213> ORGANISM: Geminivirus TYLCSV
    26 <400> SEQUENCE: 1
    27 atgccaagat caggtcgttt tagtatcaag gctaaaaatt atttccttac atatcccaaa
    29 tqtqatttaa caaaaqaaaa tqcactttcc caaataacaa acctacaaac acccacaaac
                                                                              120
    31 aaattattca tcaaaatttg cagagaacta catgaaaatg gggaacctca tctccatatt
                                                                              180
    33 ctcatccaat tcgaaggaaa atacaattgt accaatcaac gattcttcga cctggtatcc
                                                                              240
    35 ccaaccaggt cagcacattt ccatccgaac attcagggag ctaaatcgag ctccgacgtc
                                                                              300
    37 aagteetata tegacaagga eggagatgtt ettgaatggg gtaettteca gategaegga
    39 cgatctgcta ggggaggaca acagacagcc aacgacgctt acgcaaaggc aattaacgca
                                                                              420
    41 ggaagtaagt cgcaggctct tgatgtaatt aaagaattag cgcctagaga ttacgttcta
                                                                              480
    43 cattttcata atataaatag taatttagat aaggttttcc aggtgcctcc ggcaccttat
                                                                              540
    45 gtttctcctt ttttatcttc ttctttcgat caagttcctg atgaacttga acactgggtt
                                                                              600
    47 tccgagaacg tcatggatgc cgctgcgcgg
                                                                              630
    50 <210> SEQ ID NO: 2
    51 <211> LENGTH: 630
    52 <212> TYPE: DNA
    53 <213> ORGANISM: Artificial
    55 <220> FEATURE:
    56 <223> OTHER INFORMATION: TYLCSV Rep-210 modified sequence
    59 <220> FEATURE:
    60 <221> NAME/KEY: CDS
    61 <222> LOCATION: (1)..(630)
    63 <400> SEQUENCE: 2
    64 atg cct aga tcc gga agg ttt agc atc aaa gct aag aat tac ttc ttg
    65 Met Pro Arg Ser Gly Arg Phe Ser Ile Lys Ala Lys Asn Tyr Phe Leu
    66 1
    68 aca tac ccc aag tgt gac tta act aag gag aat gca ttg tcc cag ata
                                                                               96
    69 Thr Tyr Pro Lys Cys Asp Leu Thr Lys Glu Asn Ala Leu Ser Gln Ile
    70
```

Input Set : A:\PTO.TS.txt

72 act aac ttg caa act ccc act aac aag ttg ttc att aag att tgt ag	
73 Thr Asn Leu Gln Thr Pro Thr Asn Lys Leu Phe Ile Lys Ile Cys Ar	:g
74 35 40 45	
76 gaa ctt cat gag aat gga gaa cca cat ctt cat atc ttg ata cag tt	
77 Glu Leu His Glu Asn Gly Glu Pro His Leu His Ile Leu Ile Gln Ph	ne
78 50 55 60	
80 gaa ggc aag tat aac tgc acc aac caa cgt ttc ttt gac ctt gtg to	
81 Glu Gly Lys Tyr Asn Cys Thr Asn Gln Arg Phe Phe Asp Leu Val Se	er
82 65 70 75 80	)
84 cct acc aga tca gcc cat ttt cat cca aac atc cag ggt gct aag tc	g 288
85 Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Gly Ala Lys Se	er
86 85 90 95	
88 agt tca gac gtg aag tca tac att gac aaa gac ggc gat gtg ctc ga	ag 336
89 Ser Ser Asp Val Lys Ser Tyr Ile Asp Lys Asp Gly Asp Val Leu Gl	lu
90 100 105 110	
92 tgg gga act ttt cag ata gac ggt cga tcg gct aga gga ggt cag ca	aa 384
93 Trp Gly Thr Phe Gln Ile Asp Gly Arg Ser Ala Arg Gly Gly Gln Gl	ln
94 115 120 125	
96 aca get aac gat gea tac get aag get ate aac get gga tee aag te	ca 432
97 Thr Ala Asn Asp Ala Tyr Ala Lys Ala Ile Asn Ala Gly Ser Lys Se	er
98 130 135 140	
100 cag gca ctt gac gta atc aaa gag tta gct cct agg gat tat gtt c	ctt 480
101 Gln Ala Leu Asp Val Ile Lys Glu Leu Ala Pro Arg Asp Tyr Val I	
	160
104 cat ttc cat aac atc aac agc aat ttg gac aaa gtg ttc caa gtg c	cca 528
105 His Phe His Asn Ile Asn Ser Asn Leu Asp Lys Val Phe Gln Val F	
106 165 170 175	
108 ccg gct cct tac gtt tca cct ttc tta agt tct tca ttt gat cag g	gtt 576
109 Pro Ala Pro Tyr Val Ser Pro Phe Leu Ser Ser Ser Phe Asp Gln V	/al
110 180 185 190	
112 cca gat gag ctt gag cat tgg gtg tcc gaa aac gtt atg gac gcc g	gca 624
113 Pro Asp Glu Leu Glu His Trp Val Ser Glu Asn Val Met Asp Ala A	
114 195 200 205	
116 gcg cgt	630
117 Ala Arg	
118 210	
121 <210> SEQ ID NO: 3	
122 <211> LENGTH: 210	
123 <212> TYPE: PRT	•
124 <213> ORGANISM: Artificial	
126 <220> FEATURE:	
127 <223> OTHER INFORMATION: Synthetic Construct	,
129 <400> SEQUENCE: 3	·
131 Met Pro Arg Ser Gly Arg Phe Ser Ile Lys Ala Lys Asn Tyr Phe I	Leu
132 1 5 10 15 15 15 15 15 15 15 15 15 15 15 15 15	<del>-</del>
135 Thr Tyr Pro Lys Cys Asp Leu Thr Lys Glu Asn Ala Leu Ser Gln 1	(le
136 20 25 30	
139 Thr Asn Leu Gln Thr Pro Thr Asn Lys Leu Phe Ile Lys Ile Cys A	Ara
140 35 40 45	<i>3</i>
20 40 40	•

Input Set : A:\PTO.TS.txt

143																	
	Glu		His	Glu	Asn	Gly	Glu	Pro	His	Leu	His		Leu	Ile	Gln	Phe	
144	Glu	50 Glv	Lvs	Tvr	Asn	Cvs	55 Thr	Asn	Gln	Ara	Phe	60 Phe	Asp	Len	Val	Ser	
148		O <sub>1</sub>	טעב	-7-	21011	70		11011	Q111	****9	75	1110	1100	Lcu	•u=	80	
151	Pro	Thr	Arg	Ser	Ala	His	Phe	His	Pro	Asn	Ile	Gln	Gly	Ala	Lys	Ser	
152					85					90					95		
	Ser	Ser	Asp		Lys	Ser	$\mathtt{Tyr}$	Ile		Lys	Asp	Gly	Asp		Leu	Glu	
156		~7		100	<b>~</b> 1			~1	105				~1	110	~1	<b>a</b> 3 .	
	Trp	GLY		Phe	GIn	He	Asp	_	Arg	Ser	Ala	Arg	_	GIY	GIn	Gin	
160	Thr	בומ	115	Acn	Δla	Туг	Ala	120	<b>Δ</b> 1 =	Tla	Δen	בומ	125	Ser	Larg	Ser	
164	1111	130	71011	мор	mu	- 7 -	135	Lys	ALU	110	21011	140	Ory	DCI	цу	DCI	
	Gln		Leu	Asp	Val	Ile	Lys	Glu	Leu	Ala	Pro	-	Asp	Tyr	Val	Leu	
	145			_		150	•				155		-	•		160	
171	His	Phe	His	Asn	Ile	Asn	Ser	Asn	Leu	Asp	Lys	Val	Phe	Gln	Val	Pro	
172					165					170					175		
	Pro	Ala	Pro	_	Val	Ser	Pro	Phe		Ser	Ser	Ser	Phe	_	Gln	Val	
176		_		180			_		185		_			190			
	Pro	Asp		Leu	GIu	His	Trp		Ser	GIu	Asn	Val		Asp	Ala	Ala	
180	ת דת	7~~	195					200					205				
184	Ala	210															
	<210		EO TI	ON C	٠ 4												
	<21:																
189	<212	2> T:	YPE:	DNA													
	<213				Art	ific	ial										
190		3 > OI	RGAN	ISM:	Art	ific:	ial										
190 192 193	<213 <220 <223	3> OI 0> FI 3> O	RGAN: EATUI THER	ISM: RE: INFO			ial : TYI	CSV	Rep-	-210	mod:	ifie	d sec	quenc	ce		
190 192 193 196	<213 <220 <223 <220	3 > OI 0 > FI 3 > O' 0 > FI	RGAN EATUI THER EATUI	ISM: RE: INFO RE:	ORMA'			LCSV	Rep-	-210	mod:	ifie	d sed	quend	ce		
190 192 193 196 197	<213 <220 <223 <220 <225	3 > OI 0 > FI 3 > O' 0 > FI 1 > NA	RGAN: EATUI THER EATUI AME/I	ISM: RE: INFO RE: KEY:	ORMA'	rion:	: TYI	LCSV	Rep-	-210	modi	ifie	d sed	quenc	ce		
190 192 193 196 197 198	<213 <220 <223 <220 <223 <223	3 > OI 0 > FI 3 > O' 0 > FI 1 > NI 2 > LO	RGANI EATUI THER EATUI AME/I OCATI	ISM: RE: INFO RE: KEY: ION:	CDS	rion:	: TYI	LCSV	Rep-	-210	modi	ifie	d sed	quend	ce		
190 192 193 196 197 198 200	<213 <220 <223 <220 <222 <222 <400	3 > OI 0 > FI 3 > O' 0 > FI 1 > NI 2 > LO 0 > SI	RGANI EATUI THER EATUI AME/I DCATI	ISM: RE: INFO RE: KEY: ION:	CDS (1)	rion	: TYI							-		tta	48
190 192 193 196 197 198 200 201	<213 <220 <223 <223 <223 <400 atg	3 > OF 0 > FI 3 > OF 0 > FI 1 > NZ 2 > LO 0 > SI cct	RGANI EATUI EATUI AME/I OCATI EQUEI aga	ISM: RE: INFO RE: REY: ION: NCE:	CDS (1) 4 gga	rion	: TY1 30) ttt	agc	atc	aaa	gct	aag	aat	tac	ttc		48
190 192 193 196 197 198 200 201	<213 <220 <223 <222 <222 <400 atg	3 > OF 0 > FI 3 > OF 0 > FI 1 > NZ 2 > LO 0 > SI cct	RGANI EATUI EATUI AME/I OCATI EQUEI aga	ISM: RE: INFO RE: REY: ION: NCE:	CDS (1) 4 gga	rion	: TYI	agc	atc	aaa	gct	aag	aat	tac	ttc		48
190 192 193 196 197 198 200 201 202 203	<213 <220 <223 <222 <222 <400 atg Met 1	3 > OH 0 > FH 3 > OH 0 > FH 1 > NA 2 > LOH 0 > SH cct Pro	RGANI FATUR THER EATUR AME/I DCATI EQUER aga Arg	ISM: RE: INFO RE: CEY: ION: TCE: tcc Ser	CDS (1) 4 gga Gly 5	rion (6: agg Arg	: TY1 30) ttt	agc Ser	atc Ile	aaa Lys 10	gct Ala	aag Lys	aat Asn	tac Tyr	ttc Phe 15	Leu	<b>4</b> 8 96
190 192 193 196 197 198 200 201 202 203 205	<213 <220 <223 <222 <222 <400 atg Met 1 aca	3 > OI 0 > FI 3 > OO 0 > FI 1 > NI 2 > LO 0 > SI cct Pro	RGANI PHER EATUR AME/I OCATI EQUER AGA ARG	ISM: RE: INF( RE: CEY: ION: TCE: TCC Ser aag	CDS (1) 4 gga Gly 5 tgt	rion(6: agg Arg	: TYI 30) ttt Phe	agc Ser	atc Ile	aaa Lys 10 gag	gct Ala aat	aag Lys gca	aat Asn ttg	tac Tyr	ttc Phe 15 cag	Leu ata	
190 192 193 196 197 198 200 201 202 203 205	<213 <220 <223 <222 <222 <400 atg Met 1 aca	3 > OI 0 > FI 3 > OO 0 > FI 1 > NI 2 > LO 0 > SI cct Pro	RGANI PHER EATUR AME/I OCATI EQUER AGA ARG	ISM: RE: INF( RE: CEY: ION: TCE: TCC Ser aag	CDS (1) 4 gga Gly 5 tgt	rion(6: agg Arg	: TYI 30) ttt Phe tta	agc Ser	atc Ile	aaa Lys 10 gag	gct Ala aat	aag Lys gca	aat Asn ttg	tac Tyr	ttc Phe 15 cag	Leu ata	
190 192 193 196 197 198 200 201 202 203 205 206 207 209	<213 <220 <223 <222 <400 atg Met 1 aca Thr	3 > OI 0 > FI 3 > O' 0 > FI 1 > NZ 2 > LO 0 > SI cct Pro tac Tyr	RGAN: EATUR THER EATUR AME/IR CCAT: EQUER AGA Arg CCC Pro	ISM: RE: INFO RE: CEY: ION: tcc Ser aag Lys 20 caa	CDS (1) 4 gga Gly 5 tgt Cys act	agg Arg gac Asp	: TYI 30) ttt Phe tta Leu act	agc Ser act Thr	atc Ile aag Lys 25	aaa Lys 10 gag Glu ttg	gct Ala aat Asn ttc	aag Lys gca Ala att	aat Asn ttg Leu aag	tac Tyr tcc Ser 30	ttc Phe 15 cag Gln tgt	Leu ata Ile agg	
190 192 193 196 197 198 200 201 202 203 205 206 207 209 210	<213 <220 <223 <222 <400 atg Met 1 aca Thr	3 > OI 0 > FI 3 > O' 0 > FI 1 > NZ 2 > LO 0 > SI cct Pro tac Tyr	RGAN: EATUR THER EATUR AME / I DCAT: EQUER AGA Arg CCC Pro ttg Leu	ISM: RE: INFO RE: CEY: ION: tcc Ser aag Lys 20 caa	CDS (1) 4 gga Gly 5 tgt Cys act	agg Arg gac Asp	: TYI 30) ttt Phe tta Leu	agc Ser act Thr aac	atc Ile aag Lys 25	aaa Lys 10 gag Glu ttg	gct Ala aat Asn ttc	aag Lys gca Ala att	aat Asn ttg Leu aag Lys	tac Tyr tcc Ser 30	ttc Phe 15 cag Gln tgt	Leu ata Ile agg	96
190 192 193 196 197 198 200 201 202 203 205 206 207 209 210 211	<213 <220 <223 <222 <400 atg Met 1 aca Thr	3 > OI 0 > FI 3 > O' 0 > FI 1 > NA 2 > LO 0 > SI cct Pro tac Tyr aac Asn	RGAN: EATUR THER EATUR AME/I DCAT: EQUER AGA Arg CCC Pro ttg Leu 35	ISM: RE: INFO RE: CEY: ION: tcc Ser aag Lys 20 caa Gln	CDS (1) 4 gga Gly 5 tgt Cys act	agg Arg gac Asp	ttt Phe tta Leu act	agc Ser act Thr aac Asn 40	atc Ile aag Lys 25 aag Lys	aaa Lys 10 gag Glu ttg Leu	gct Ala aat Asn ttc Phe	aag Lys gca Ala att Ile	aat Asn ttg Leu aag Lys 45	tac Tyr tcc Ser 30 att	ttc Phe 15 cag Gln tgt Cys	ata Ile agg Arg	96 144
190 192 193 196 197 198 200 201 202 203 205 206 207 209 210 211 213	<213 <220 <223 <222 <400 atg Met 1 aca Thr act Thr	3 > OI 0 > FI 3 > O' 0 > FI 1 > NA 2 > LO 0 > SI cct Pro tac Tyr aac Asn	RGAN: EATUR THER EATUR AME/I DCAT: EQUER AGA Arg CCC Pro ttg Leu 35 cac	ISM: RE: INFO RE: CEY: CON: tcc Ser aag Lys caa Gln gag	CDS (1) 4 gga Gly 5 tgt Cys act Thr	agg Arg gac Asp ccc Pro	: TYI 30) ttt Phe tta Leu act Thr	agc Ser act Thr aac Asn 40 cca	atc Ile aag Lys 25 aag Lys	aaa Lys 10 gag Glu ttg Leu	gct Ala aat Asn ttc Phe	aag Lys gca Ala att Ile	aat Asn ttg Leu aag Lys 45 ttg	tac Tyr tcc Ser 30 att Ile	ttc Phe 15 cag Gln tgt Cys	Leu ata Ile agg Arg	96
190 192 193 196 197 198 200 201 202 203 205 206 207 209 210 211 213 214	<213 <220 <223 <222 <400 atg Met 1 aca Thr act Thr	3 > OI 0 > FI 3 > O' 0 > FI 1 > NX 2 > LO 0 > SI cct Pro tac Tyr aac Asn ctt Leu	RGAN: EATUR THER EATUR AME/I DCAT: EQUER AGA Arg CCC Pro ttg Leu 35 cac	ISM: RE: INFO RE: CEY: CON: tcc Ser aag Lys caa Gln gag	CDS (1) 4 gga Gly 5 tgt Cys act Thr	agg Arg gac Asp ccc Pro	ttt Phe tta Leu act Thr	agc Ser act Thr aac Asn 40 cca	atc Ile aag Lys 25 aag Lys	aaa Lys 10 gag Glu ttg Leu	gct Ala aat Asn ttc Phe	aag Lys gca Ala att Ile atc	aat Asn ttg Leu aag Lys 45 ttg	tac Tyr tcc Ser 30 att Ile	ttc Phe 15 cag Gln tgt Cys	Leu ata Ile agg Arg	96 144
190 192 193 196 197 198 200 201 202 203 205 206 207 209 210 211 213 214 215	<213 <220 <222 <222 <400 atg Met 1 aca Thr act Thr gaa Glu	3 > OI 0 > FI 3 > O' 0 > FI 1 > NX 2 > LO 0 > SI cct Pro tac Tyr aac Asn ctt Leu 50	RGANI EATUR THER EATUR AME/I CCATI EQUER AGA CCC Pro ttg Leu 35 CaC His	ISM: RE: INFO RE: CEY: ION: tcc Ser aag Lys 20 caa Gln gag Glu	CDS (1) 4 gga Gly 5 tgt Cys act Thr aat Asn	agg Arg gac Asp ccc Pro	ttt Phe tta Leu act Thr gaa Glu 55	agc Ser act Thr aac Asn 40 cca Pro	atc Ile aag Lys 25 aag Lys cat His	aaa Lys 10 gag Glu ttg Leu ctt	gct Ala aat Asn ttc Phe cat His	aag Lys gca Ala att Ile atc Ile 60	aat Asn ttg Leu aag Lys 45 ttg Leu	tac Tyr tcc Ser 30 att Ile ata Ile	ttc Phe 15 cag Gln tgt Cys cag Gln	Leu ata Ile agg Arg ttc Phe	96 144 192
190 192 193 196 197 198 200 201 202 203 205 206 207 209 210 211 213 214 215 217	<213 <220 <222 <222 <400 atg Met 1 aca Thr act Thr gaa Glu gaa	3 > OI 0 > FI 3 > O' 0 > FI 1 > NI 2 > LO 0 > SI 0 CCt Pro tac Tyr aac Asn ctt Leu 50 ggc	RGAN: EATUR THER EATUR AME/I CCAT: EQUER AGA Arg CCC Pro ttg Leu 35 Cac His	ISM: ISM: INFO RE: CEY: ION: CEC Ser aag Lys 20 caa Gln gag Glu tat	CDS (1) 4 gga Gly 5 tgt Cys act Thr aat Asn	agg Arg gac Asp ccc Pro gga Gly	ttt Phe tta Leu act Thr gaa Glu 55 acc	agc Ser act Thr aac Asn 40 cca Pro	atc Ile aag Lys 25 aag Lys cat His	aaa Lys 10 gag Glu ttg Leu ctt Leu	gct Ala aat Asn ttc Phe cat His	aag Lys gca Ala att Ile atc Ile 60 ttt	aat Asn ttg Leu aag Lys 45 ttg Leu	tac Tyr tcc Ser 30 att Ile ata Ile	ttc Phe 15 cag Gln tgt Cys cag Gln	Leu ata Ile agg Arg ttc Phe tcc	96 144
190 192 193 196 197 198 200 201 202 203 205 206 207 210 211 213 214 215 217 218	<213 <220 <222 <222 <400 atg Met 1 aca Thr act Thr gaa Glu gaa Glu	3 > OI 0 > FI 3 > O' 0 > FI 1 > NI 2 > LO 0 > SI 0 CCt Pro tac Tyr aac Asn ctt Leu 50 ggc	RGAN: EATUR THER EATUR AME/I CCAT: EQUER AGA Arg CCC Pro ttg Leu 35 Cac His	ISM: ISM: INFO RE: CEY: ION: ICE: ICC Ser aag Lys 20 caa Gln gag Glu tat	CDS (1) 4 gga Gly 5 tgt Cys act Thr aat Asn	agg Arg gac Asp ccc Pro gga Gly	ttt Phe tta Leu act Thr gaa Glu 55	agc Ser act Thr aac Asn 40 cca Pro	atc Ile aag Lys 25 aag Lys cat His	aaa Lys 10 gag Glu ttg Leu ctt Leu	gct Ala aat Asn ttc Phe cat His	aag Lys gca Ala att Ile atc Ile 60 ttt	aat Asn ttg Leu aag Lys 45 ttg Leu	tac Tyr tcc Ser 30 att Ile ata Ile	ttc Phe 15 cag Gln tgt Cys cag Gln	Leu ata Ile agg Arg ttc Phe tcc Ser	96 144 192
190 192 193 196 197 198 200 201 202 203 205 206 207 210 211 213 214 215 217 218 219	<213 <220 <222 <222 <400 atg Met 1 aca Thr act Thr gaa Glu gaa Glu 65	3 > OI 0 > FI 3 > OI 0 > FI 1 > NI 2 > LO 0 > SI cct Pro tac Tyr aac Asn ctt Leu 50 ggc Gly	RGAN: EATUR THER EATUR AME/R CCAT: EQUER Arg CCC Pro ttg Leu 35 Cac His aag Lys	ISM: RE: INFO RE: CEY: CCY: CCC Ser  aag Lys Caaa Gln  gag Glu tat Tyr	CDS (1) 4 gga Gly 5 tgt Cys act Thr aat Asn aac	agg Arg gac Asp ccc Pro gga Gly tgc Cys 70	ttt Phe tta Leu act Thr gaa Glu 55 acc Thr	agc Ser act Thr aac Asn 40 cca Pro aac Asn	atc Ile aag Lys 25 aag Lys cat His caa Gln	aaa Lys 10 gag Glu ttg Leu ctt Leu cgt Arg	gct Ala aat Asn ttc Phe cat His ttc Phe 75	aag Lys gca Ala att Ile atc Ile 60 ttt Phe	aat Asn ttg Leu aag Lys 45 ttg Leu gac Asp	tac Tyr tcc Ser 30 att Ile ata Ile ctt Leu	ttc Phe 15 cag Gln tgt Cys cag Gln gtg Val	Leu ata Ile agg Arg ttc Phe tcc Ser 80	96 144 192 240
190 192 193 196 197 198 200 201 202 203 205 206 207 210 211 213 214 215 217 218 219 221	<213 <220 <222 <222 <400 atg Met 1 aca Thr act Thr gaa Glu gaa Glu 65 cct	3 > OI 0 > FI 3 > OI 0 > FI 1 > NI 2 > LO 0 > SI cct Pro tac Tyr aac Asn ctt Leu 50 ggc Gly acc	RGAN: EATUR THER EATUR AME/I CCAT: EQUER Arg CCC Pro ttg Leu 35 Cac His aag Lys	ISM: RE: INFO RE: INFO RE: ICEY: ICEC Ser aag Lys 20 caa Gln gag Glu tat Tyr tca	CDS (1) 4 gga Gly 5 tgt Cys act Thr aat Asn aac Asn	agg Arg gac Asp ccc Pro gga Gly tgc Cys 70 cat	ttt Phe tta Leu act Thr gaa Glu 55 acc	agc Ser act Thr aac Asn 40 cca Pro aac Asn	atc Ile aag Lys 25 aag Lys cat His caa Gln	aaa Lys 10 gag Glu ttg Leu ctt Leu cgt Arg	gct Ala aat Asn ttc Phe cat His ttc Phe 75 atc	aag Lys gca Ala att Ile atc Ile 60 ttt Phe	aat Asn ttg Leu aag Lys 45 ttg Leu gac Asp	tac Tyr tcc Ser 30 att Ile ata Ile ctt Leu	ttc Phe 15 cag Gln tgt Cys cag Gln gtg Val	Leu ata Ile agg Arg ttc Phe tcc Ser 80 tcg	96 144 192

Input Set : A:\PTO.TS.txt

223		4		- 4	85			- 4 4		90					95		226	
							tac										336	
	ser	Ser	Asp		гла	Ser	Tyr	тте		гуѕ	Asp	GIY	Asp		ьeu	GIU		
227				100					105	<b>.</b>				110			204	
							gac										384	
	Trp	GIY		Pne	GIN	тте	Asp	_	Arg	ser	Ата	Arg		GIĀ	GIII	GIII		
231			115					120					125				422	
		_		-	-		gct	_	_			-					432	
	Thr		Asn	Asp	Ala	ıyr	Ala	гÀг	Ala	тте	ASI		GIĀ	ser	ьуѕ	ser		
235	~~~	130	att	~~~	~+ ·	250	135	~~~	++-	~a+	aat	140	ant.	+ = +	~++	at t	480	
	_	_		_	_		aaa			_							400	
	145	ALA	neu	Asp	vai	150	Lys	GIU	ьец	AIA	155	Arg	Asp	TYL	vai	160		
		++0	ast	220	ata		200	22 <b>+</b>	++~	a a a		ata	++0	caa	ata		528	
							agc Ser		_	_							520	
243	птъ	FIIE	птэ	ASII	165	ASII	SET	ASII	шец	170	цуъ	vai	FIIC	GIII	175	FIO		
	aca	act	aat	tad		tra	cct	ita	tta		tot	tca	+++	cat	-	att	576	
							Pro										370	
247	110	ALG	110	180	vai	DCI	110	1110	185	DCI	DCL	DCI	1110	190	0111	vul		
	cca	σat	gag		aaa	cat	tgg	ata		gaa	aac	att	ato		acc	gca	624	
							Trp										021	
251	110	1155	195					200	501	J_ u			205					
	gcc	cat			•												630	
	Ala	_																
255		210																
258	<210	0 > SI	EO II	ONO:	: 5													
		0> SI 1> LI																
259	<21	0> SI 1> LI 2> T	ENGT	H: 2														
259 260	<213	1> L	ENGTI YPE :	H: 21	10	ific:	ial											
259 260 261	<213 <213 <213	1> LI 2> T	ENGTI YPE : RGAN :	H: 21 PRT ISM:	10	ific	ial											
259 260 261 263	<213 <213 <223	1> L1 2> T3 3> O1 0> F1	ENGTI YPE : RGAN : EATUI	H: 21 PRT ISM: RE:	lO Art:		ial : Syr	thet	cic (	Const	truci							
259 260 261 263 264	<213 <213 <213 <220 <223	1> L1 2> T3 3> O1 0> F1	ENGTI YPE : RGAN : EATUI THER	H: 21 PRT ISM: RE: INFO	Art: ORMA			nthet	ic (	Const	truct							
259 260 261 263 264 266	<213 <213 <213 <220 <223 <400	1 > L1 2 > T 3 > O1 0 > F1 3 > O1 0 > S1	ENGTI YPE : RGAN: EATUI THER EQUEI	H: 21 PRT ISM: RE: INFO	Art: ORMA:	rion:							Asn	Tyr	Phe	Leu		
259 260 261 263 264 266 268 269	<21: <21: <22: <22: <40: Met 1	1 > L1 2 > T1 3 > O1 0 > F1 3 > O1 0 > S1 Pro	ENGTI YPE: RGAN: EATUI THER EQUEI Arg	H: 21 PRT ISM: RE: INFO	Art: ORMA: 5 Gly 5	rion Arg	: Syr	Ser	Ile	Lys 10	Ala	Lys			15			
259 260 261 263 264 266 268 269	<21: <21: <22: <22: <40: Met 1	1 > L1 2 > T1 3 > O1 0 > F1 3 > O1 0 > S1 Pro	ENGTI YPE: RGAN: EATUI THER EQUEI Arg	H: 21 PRT ISM: RE: INFO	Art: ORMA: 5 Gly 5	rion Arg	: Syı	Ser	Ile	Lys 10	Ala	Lys			15			
259 260 261 263 264 266 268 269	<21: <21: <22: <22: <40: Met 1	1 > L1 2 > T1 3 > O1 0 > F1 3 > O1 0 > S1 Pro	ENGTI YPE: RGAN: EATUI THER EQUEI Arg	H: 21 PRT ISM: RE: INFO	Art: ORMA: 5 Gly 5	rion Arg	: Syr	Ser	Ile	Lys 10	Ala	Lys			15			
259 260 261 263 264 266 268 269 272 273	<21: <21: <22: <22: <40: Met 1 Thr	1> L1 2> T3 3> O1 0> F1 0> S1 Pro	ENGTI YPE: RGAN: EATUI THER EQUEI Arg Pro	H: 21 PRT ISM: RE: INFO NCE: Ser Lys 20	Art: DRMAG 5 Gly 5 Cys	rion Arg Asp	: Syr	Ser Thr	Ile Lys 25	Lys 10 Glu	Ala Asn	Lys Ala	Leu	Ser 30	15 Gln	Ile		
259 260 261 263 264 266 268 269 272 273 276 277	<21: <21: <22: <22: <40: Met 1 Thr	1 > L1 2 > T; 3 > O1 0 > F1 3 > O; 0 > S1 Pro Tyr Asn	ENGTH YPE: RGAN: EATUH THER EQUEN Arg Pro Leu 35	H: 2: PRT ISM: RE: INFO NCE: Ser Lys 20 Gln	Art: DRMAT 5 Gly 5 Cys Thr	Arg Asp Pro	Phe Leu Thr	Ser Thr Asn 40	Ile Lys 25 Lys	Lys 10 Glu Leu	Ala Asn Phe	Lys Ala Ile	Leu Lys 45	Ser 30 Ile	15 Gln Cys	Ile Arg		
259 260 261 263 264 266 268 272 273 276 277 280	<21: <21: <22: <22: <40: Met 1 Thr	1 > L1 2 > T; 3 > O1 0 > F1 3 > O; 0 > S1 Pro Tyr Asn	ENGTH YPE: RGAN: EATUH THER EQUEN Arg Pro Leu 35	H: 2: PRT ISM: RE: INFO NCE: Ser Lys 20 Gln	Art: DRMAT 5 Gly 5 Cys Thr	Arg Asp Pro	Phe Leu Thr	Ser Thr Asn 40	Ile Lys 25 Lys	Lys 10 Glu Leu	Ala Asn Phe	Lys Ala Ile Ile	Leu Lys 45	Ser 30 Ile	15 Gln Cys	Ile Arg		
259 260 261 263 264 266 268 272 273 276 277 280 281	<21: <21: <22: <22: <400 Met 1 Thr Glu	1 > Li 2 > TY 3 > OI 0 > FI 3 > OY 0 > SI Pro Tyr Asn Leu 50	ENGTH YPE: RGAN: EATUH THER EQUEN Arg Pro Leu 35 His	H: 21 PRT ISM: RE: INFO NCE: Ser Lys 20 Gln Glu	Art: DRMA: 5 Gly 5 Cys Thr	Arg Asp Pro Gly	Phe Leu Thr Glu 55	Ser Thr Asn 40 Pro	Ile Lys 25 Lys His	Lys 10 Glu Leu Leu	Ala Asn Phe His	Lys Ala Ile Ile 60	Leu Lys 45 Leu	Ser 30 Ile Ile	15 Gln Cys Gln	Ile Arg Phe		
259 260 261 263 264 266 269 272 273 276 280 281 284	<21: <21: <22: <22: <400 Met 1 Thr Glu Glu	1 > Li 2 > TY 3 > OI 0 > FI 3 > OY 0 > SI Pro Tyr Asn Leu 50	ENGTH YPE: RGAN: EATUH THER EQUEN Arg Pro Leu 35 His	H: 21 PRT ISM: RE: INFO NCE: Ser Lys 20 Gln Glu	Art: DRMA: 5 Gly 5 Cys Thr	Arg Asp Pro Gly Cys	Phe Leu Thr	Ser Thr Asn 40 Pro	Ile Lys 25 Lys His	Lys 10 Glu Leu Leu	Ala Asn Phe His	Lys Ala Ile Ile 60	Leu Lys 45 Leu	Ser 30 Ile Ile	15 Gln Cys Gln	Ile Arg Phe Ser		
259 260 261 263 264 266 268 272 273 276 277 280 281 284 285	<21: <21: <22: <22: <400 Met 1 Thr Glu Glu 65	1 > Li 2 > TY 3 > OI 0 > FI 3 > OY 0 > SI Pro Tyr Asn Leu 50 Gly	ENGTH YPE: RGAN: REATUR THER EQUEN Arg Pro Leu 35 His	PRT ISM: RE: INFO NCE: Ser Lys 20 Gln Glu Tyr	Art: DRMAT 5 Gly 5 Cys Thr Asn	Arg Asp Pro Gly Cys 70	Phe Leu Thr Glu 55 Thr	Ser Thr Asn 40 Pro Asn	Ile Lys 25 Lys His Gln	Lys 10 Glu Leu Leu	Ala Asn Phe His Phe 75	Lys Ala Ile Ile 60 Phe	Leu Lys 45 Leu Asp	Ser 30 Ile Ile Leu	15 Gln Cys Gln Val	Ile Arg Phe Ser 80		
259 260 261 263 264 266 268 272 273 276 277 280 281 284 285 288	<21: <21: <22: <22: <400 Met 1 Thr Glu Glu 65	1 > Li 2 > TY 3 > OI 0 > FI 3 > OY 0 > SI Pro Tyr Asn Leu 50 Gly	ENGTH YPE: RGAN: REATUR THER EQUEN Arg Pro Leu 35 His	PRT ISM: RE: INFO NCE: Ser Lys 20 Gln Glu Tyr	Art: DRMAT 5 Gly 5 Cys Thr Asn Asn	Arg Asp Pro Gly Cys 70	Phe Leu Thr Glu 55	Ser Thr Asn 40 Pro Asn	Ile Lys 25 Lys His Gln	Lys 10 Glu Leu Leu Arg	Ala Asn Phe His Phe 75	Lys Ala Ile Ile 60 Phe	Leu Lys 45 Leu Asp	Ser 30 Ile Ile Leu	15 Gln Cys Gln Val Lys	Ile Arg Phe Ser 80		
259 260 261 263 264 266 268 272 273 276 277 280 281 284 285 288 289	<21: <21: <22: <22: <400 Met 1 Thr Thr Glu Glu 65 Pro	1 > Li 2 > T' 3 > OI 0 > FI 3 > O' 0 > FI 7 Pro Tyr Asn Leu 50 Gly Thr	ENGTH YPE: RGAN: RGAN: PHER EQUEN Arg Pro Leu 35 His Lys	PRT ISM: RE: INFO NCE: Ser Lys 20 Gln Glu Tyr Ser	Art: DRMAT 5 Gly 5 Cys Thr Asn Asn Ala 85	Arg Asp Pro Gly Cys 70 His	Phe Leu Thr Glu 55 Thr	Ser Thr Asn 40 Pro Asn His	Ile Lys 25 Lys His Gln	Lys 10 Glu Leu Leu Arg Asn 90	Ala Asn Phe His Phe 75 Ile	Lys Ala Ile Ile 60 Phe Gln	Leu Lys 45 Leu Asp	Ser 30 Ile Ile Leu Ala	15 Gln Cys Gln Val Lys 95	Ile Arg Phe Ser 80 Ser		
259 260 261 263 264 268 269 272 273 276 281 284 285 288 289 292	<21: <21: <22: <22: <400 Met 1 Thr Thr Glu Glu 65 Pro	1 > Li 2 > T' 3 > OI 0 > FI 3 > O' 0 > FI 7 Pro Tyr Asn Leu 50 Gly Thr	ENGTH YPE: RGAN: RGAN: PHER EQUEN Arg Pro Leu 35 His Lys	PRT ISM: RE: INFO NCE: Ser Lys 20 Gln Glu Tyr Ser Val	Art: DRMAT 5 Gly 5 Cys Thr Asn Asn Ala 85 Lys	Arg Asp Pro Gly Cys 70 His	Phe Leu Thr Glu 55 Thr	Ser Thr Asn 40 Pro Asn His	Ile Lys 25 Lys His Gln Pro Asp	Lys 10 Glu Leu Leu Arg Asn 90	Ala Asn Phe His Phe 75 Ile	Lys Ala Ile Ile 60 Phe Gln	Leu Lys 45 Leu Asp	Ser 30 Ile Ile Leu Ala Val	15 Gln Cys Gln Val Lys 95	Ile Arg Phe Ser 80 Ser		
259 260 261 263 264 266 268 269 272 273 276 281 284 285 288 289 292 293	<21: <21: <22: <22: <400 Met 1 Thr Thr Glu Glu 65 Pro Ser	1 > Li 2 > T' 3 > OI 0 > FI 3 > O' 0 > SI Pro Tyr Asn Leu 50 Gly Thr	ENGTH YPE: RGAN: RGAN: PHER EQUEN Arg Pro Leu 35 His Lys Arg	PRT ISM: RE: INFO NCE: Ser Lys 20 Gln Glu Tyr Ser Val	Art: DRMAT 5 Gly 5 Cys Thr Asn Asn Ala 85 Lys	Arg Asp Pro Gly Cys 70 His	Phe Leu Thr Glu 55 Thr Phe	Ser Thr Asn 40 Pro Asn His	Lys 25 Lys His Gln Pro Asp 105	Lys 10 Glu Leu Leu Arg Asn 90 Lys	Ala Asn Phe His Phe 75 Ile Asp	Lys Ala Ile Ile 60 Phe Gln Gly	Leu Lys 45 Leu Asp Gly	Ser 30 Ile Ile Leu Ala Val	15 Gln Cys Gln Val Lys 95 Leu	Ile Arg Phe Ser 80 Ser Glu		
259 260 261 263 264 266 268 272 273 276 277 280 281 285 288 289 292 293 296	<21: <21: <22: <22: <400 Met 1 Thr Thr Glu Glu 65 Pro Ser	1 > Li 2 > T' 3 > OI 0 > FI 3 > O' 0 > SI Pro Tyr Asn Leu 50 Gly Thr	ENGTHYPE: RGAN: RGAN: FATURE REQUENT Arg Pro Leu 35 His Lys Arg Asp Thr	PRT ISM: RE: INFO NCE: Ser Lys 20 Gln Glu Tyr Ser Val	Art: DRMAT 5 Gly 5 Cys Thr Asn Asn Ala 85 Lys	Arg Asp Pro Gly Cys 70 His	Phe Leu Thr Glu 55 Thr	Ser Thr Asn 40 Pro Asn His Ile Gly	Lys 25 Lys His Gln Pro Asp 105	Lys 10 Glu Leu Leu Arg Asn 90 Lys	Ala Asn Phe His Phe 75 Ile Asp	Lys Ala Ile Ile 60 Phe Gln Gly	Leu Lys 45 Leu Asp Gly Asp	Ser 30 Ile Ile Leu Ala Val	15 Gln Cys Gln Val Lys 95 Leu	Ile Arg Phe Ser 80 Ser Glu		
259 260 261 263 264 268 269 272 273 276 281 284 285 288 292 293 296 297	<21: <21: <22: <22: <400 Met 1 Thr Glu Glu 65 Pro Ser Trp	1 > Li 2 > T' 3 > Oi 3 > Oi 0 > Fi 3 > O' 7 Pro Tyr Asn Leu 50 Gly Thr Ser Gly	ENGTHYPE: RGAN: RGAN: FHER EQUEN Arg Pro Leu 35 His Lys Arg Asp Thr	PRT ISM: RE: INFO NCE: Ser Lys 20 Gln Glu Tyr Ser Val 100 Phe	Art: DRMAT 5 Gly 5 Cys Thr Asn Ala 85 Lys Gln	Arg Asp Pro Gly Cys 70 His ser	Phe Leu Thr Glu 55 Thr Phe	Ser Thr Asn 40 Pro Asn His Ile Gly 120	Ile Lys 25 Lys His Gln Pro Asp 105 Arg	Lys 10 Glu Leu Leu Arg Asn 90 Lys Ser	Ala Asn Phe His Phe 75 Ile Asp Ala	Lys Ala Ile Ile 60 Phe Gln Gly Arg	Leu Lys 45 Leu Asp Gly Asp	Ser 30 Ile Ile Leu Ala Val 110 Gly	15 Gln Cys Gln Val Lys 95 Leu Gln	Ile Arg Phe Ser 80 Ser Glu Gln		

Input Set : A:\PTO.TS.txt

301		130					135					140					
304	Gln	Ala	Leu	Asp	Val	Ile	Lys	Glu	Leu	Ala	Pro	Arg	Asp	Tyr	Val	Leu	-
305	145					150					155					160	
308	His	Phe	His	Asn	Ile	Asn	Ser	Asn	Leu	Asp	Lys	Val	Phe	Gln	Val	Pro	
309					165					170	•				175		
	Pro	Ala	Pro	Tvr		Ser	Pro	Phe	Leu		Ser	Ser	Phe	Asp	Gln	Val	
313				180					185					190			
	Pro	Acn	Glu		Glu	Hic	Trn	Val		Glu	Δan	Va l	Met	Asp	Δla	Δla	
317	110	пор	195	пси	Olu	111.5	110	200	DCI	OIU	11011	vui	205	1101	1114	1114	
	Ala	7~~	193					200					205				
	міа	210															
321	-21		- TI	) NO													
	<210													<b>\</b>			
	<21				/4												
	<212																
	<21:				Art:	liic:	ıaı										
	<220								_	_				_			
					ORMA'	rion:	: TYI	LCSV	Coat	t Pro	otei	n mod	difie	ed se	equei	nce	
	<220																
	<22:																
	<222					(7	74)										
	<400										-						
														gtg			48
339	Met	Pro	Lys	Arg	Thr	Gly	Asp	Ile	Leu	Ile	Ser	Thr	Pro	Val	Ser	Lys	
340	1				5					10					15		
342	gtg	cgt	agg	aga	ctt	aac	ttt	gac	tct	ccg	tac	acc	tct	cgt	gca	gct	96
343	Val	Arg	Arg	Arg	Leu	Asn	Phe	Asp	Ser	Pro	Tyr	Thr	Ser	Arg	Ala	Ala	
344				20					25					30			
346	qct	ccc	aca	gtc	cag	ggc	att	aag	agg	cga	tct	tgg	aca	tac	aga	cct	144
														Tyr			
348			35			-		40	J	_		-	45	-	_		
350	atq	tac	agg	aaa	ccq	aqq	atq	tat	agg	atq	tat	cqt	aqc	cca	qat	qtq	192
														Pro			
352		50	,	•			55	•	,		•	60			•		
	cct		aat.	tac	gaa	gga	ccc	tac	aaσ	ata	caa	tca	tat	gag	caa	cat	240
														Glu			
356			1	-7-		70		-1-	-1-		75		-1-			80	
		gat	at.a.	aaσ	cac		gga	at.t.	at.t	cat.		at.t.	tet	gat	ata		288
														Asp			
360	пор	пор	vul	<b>L</b> y5	85		017	VUI	V 4.1	90	Cyb	• • • • • • • • • • • • • • • • • • • •	501	110p	95		
	202	aat	tas	aat		act	a = a	200	ata		224	aat	tta	tgt		220	336
														Cys			330
364	Arg	GIY	SCI	100	116	1111	птэ	AI 9	105	Gry	цуз	Arg	FIIC	110	110	цуз	
						~~+					~~~	~~~	22+		224	222	384
														atc			304
	ser	тте	_	тте	пеп	GIY	пλя		ттр	Mec	Asp	GIU	125	Ile	пур	пур	
368			115					120	<b>L</b> L -					~~+		200	420
														gat			432
	GIN		Hls	ınr	Asn	GIN		мет	rne	rne	ьеи		arg	Asp	arg	arg	
372		130					135					140					
374	cca	tac	gga	acc	agc	cca	atg	gac	ttc	ggc	cag	gtg	ttt	aat	atg	ttc	480

Input Set : A:\PTO.TS.txt

Output Set: N:\CRF4\11282005\J557288.raw

#### Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:2,3,4,5,6,7,8,9,10,11

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/557,288

DATE: 11/28/2005 TIME: 13:16:20

Input Set : A:\PTO.TS.txt

Output Set: N:\CRF4\11282005\J557288.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date